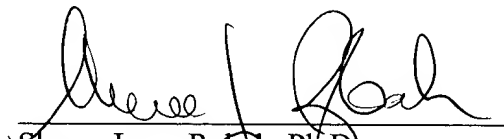


If any matters remain before the present application is examined on the merits, the Examiner is invited to telephone the undersigned at the telephone number listed below.

Respectfully submitted,

KLARQUIST SPARKMAN, LLP

By


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**Marked-up Version of Amended Specification
Pursuant to 37 C.F.R. §§ 1.121(b)-(c)**

Replace the paragraph on page 3, lines 26-31, with the following:

FIG. 1 is a sequence comparison of an EDA1-II (EDA) (SEQ ID NO 2) and Tabby (Ta) (SEQ ID NO 2) proteins. Amino acid identities are indicated by an asterisk (*). The transmembrane domain is boxed. A vertical line designates the start of the protein sequence unique to isoform II. The Gly-X-Y domain is indicated by boldface type, with the 2-amino acid interruption indicated by shadowed lettering. A blackened circle is shown above two potential N-linked glycosylation sites, and three C-terminal cysteines are indicated by underlining and boldface type.

Replace the paragraph on page 4, lines 7-11, with the following:

FIG. 4 is a comparison of the sequences of the central β -sheet of EDA1-II (amino acids 291-309 of SEQ ID NO 2) compared with human tumor necrosis factor (Hu TNF, SEQ ID NO 123), lymphotoxin α (LT α , SEQ ID NO 124), lymphotoxin β (LT β , SEQ ID NO 125), FAS (SEQ ID NO 126), and CD40-L (ligand, SEQ ID NO 127), which are all members of the TNF family of proteins. One dot over a column indicates conservation across all sequences. Two dots over a column indicates the G(x)Y (glycine and tyrosine residues) identified in all the TNF related proteins.

Insert the following paragraphs on page 5, line 33:

SEQ ID NO 123 shows a portion of a human tumor necrosis factor protein.

SEQ ID NO 124 shows a portion of a human lymphotoxin α protein.

SEQ ID NO 125 shows a portion of a human lymphotoxin β protein.

SEQ ID NO 126 shows a portion of a human FAS protein.

SEQ ID NO 127 shows a portion of a human CD40-L protein.

Replace the paragraph on page 20, lines 9-14, with the following:

The EDA1-II cDNA (SEQ ID NO 1) encodes a 391 residue protein (SEQ ID NO 2), 256 amino acids of which are encoded by new exons. EDA1-II is 94% identical to Tabby (SEQ ID NO 4), and includes a collagen-like domain with 19 repeats of a Gly-X-Y motif, interrupted by

two amino acids between repeats 11 and 12 (FIG. 1). The full-length EDA1-II transcript can include a longer 3' UTR, because no polyadenylation signal sequence was identified, and Northern analysis indicates the transcript is 5-6 kb in length. The *Tabby* transcript is also 5-6 kb in length and has a 3' UTR of approximately 3.5 kb.